



SEQUENCE LISTING

<110> Busfield, Samantha J.  
<120> NOVEL MOLECULES OF THE  
HERPESVIRUS-ENTRY-MEDIATOR-RELATED  
PROTEIN FAMILY AND USES THEREOF

<130> MBIO98-061CP1CN1(M)

<140> 09/934,289  
<141> 2001-08-21

<150> US 09/342,767  
<151> 1999-06-29

<150> US 09/146,950  
<151> 1998-09-03

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ctgctggagt	tcctcctgct	agctgggttc	ccgagctgcc	ggtctgagcc	tgaggc atg	299
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Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro Arg	
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acc gac gtc ttg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc ccc	395
Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala Pro	
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tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca gtg	443
Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val	
35 40 45	

ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag gag	491
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Gly	Ser	Glu	Cys	Cys	Pro	Lys	Cys	Ser	Pro	Gly	Tyr	Arg	Val	Lys	Glu	
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Thr	Tyr	Ile		His	Leu	Asn	Gly	Leu	Ser	Lys	Cys	Leu	Gln	Cys	Gln	
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Met	Cys	Asp	Pro	Ala	Met	Gly	Leu	Arg	Ala	Ser	Arg	Asn	Cys	Ser	Arg	
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Thr	Glu	Asn	Ala	Val	Cys	Gly	Cys	Ser	Pro	Gly	His	Phe	Cys	Ile	Val	
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Gln	Asp	Gly	Asp	His	Cys	Ala	Ala	Cys	Arg	Ala	Tyr	Ala	Thr	Ser	Ser	
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Pro	Gly	Gln	Arg	Val	Gln	Lys	Gly	Gly	Thr	Glu	Ser	Gln	Asp	Thr	Leu	
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Cys	Gln	Asn	Cys	Pro	Pro	Gly	Thr	Phe	Ser	Pro	Asn	Gly	Thr	Leu	Glu	
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Glu	Cys	Gln	His	Gln	Thr	Asn	Arg	Ala	Trp	Lys	Ser	Gln	Thr	Asp	Leu	
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<213> Homo sapiens

<220>

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<222> (1)...(38)

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Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
      -5      1      5      10
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
      15      20      25
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
      30      35      40
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
      45      50      55
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
      60      65      70
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
      75      80      85      90
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
      95      100      105
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
      110      115      120
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
      125      130      135
Glu Glu Cys Gln His Gln Thr Asn Arg Ala Trp Lys Ser Gln Thr Asp
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Leu
155
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<222> (1)...(579)

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Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
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aga acc gac gtc ttg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc      96
Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
      20      25      30

ccc tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca      144
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
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gtg ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag      192
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Glu	Ala	Cys	Gly	Glu	Leu	Thr	Gly	Thr	Val	Cys	Glu	Pro	Cys	Pro	Pro		
65					70				75						80		
ggc	acc	tac	att	gcc	cac	ctc	aat	ggc	cta	agc	aag	tgt	ctg	cag	tgc	288	
Gly	Thr	Tyr	Ile	Ala	His	Leu	Asn	Gly	Leu	Ser	Lys	Cys	Leu	Gln	Cys		
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caa	atg	tgt	gac	cca	gcc	atg	ggc	ctg	cgc	gcg	agc	cgg	aac	tgc	tcc	336	
Gln	Met	Cys	Asp	Pro	Ala	Met	Gly	Leu	Arg	Ala	Ser	Arg	Asn	Cys	Ser		
			100					105					110				
agg	aca	gag	aac	gcc	gtg	tgt	ggc	tgc	agc	cca	ggc	cac	ttc	tgc	atc	384	
Arg	Thr	Glu	Asn	Ala	Val	Cys	Gly	Cys	Ser	Pro	Gly	His	Phe	Cys	Ile		
			115				120					125					
gtc	cag	gac	ggg	gac	cac	tgc	gcc	gcg	tgc	cgc	gct	tac	gcc	acc	tcc	432	
Val	Gln	Asp	Gly	Asp	His	Cys	Ala	Ala	Cys	Arg	Ala	Tyr	Ala	Thr	Ser		
	130					135					140						
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Ser	Pro	Gly	Gln	Arg	Val	Gln	Lys	Gly	Gly	Thr	Glu	Ser	Gln	Asp	Thr		
145					150					155					160		
ctg	tgt	cag	aac	tgc	ccc	ccg	ggg	acc	ttc	tct	ccc	aat	ggg	acc	ctg	528	
Leu	Cys	Gln	Asn	Cys	Pro	Pro	Gly	Thr	Phe	Ser	Pro	Asn	Gly	Thr	Leu		
				165					170					175			
gag	gaa	tgt	cag	cac	cag	acc	aac	cga	gct	tgg	aaa	agt	cag	aca	gac	576	
Glu	Glu	Cys	Gln	His	Gln	Thr	Asn	Arg	Ala	Trp	Lys	Ser	Gln	Thr	Asp		
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Leu																	

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			20					25					30				
Thr	Gly	Thr	Val	Cys	Glu	Pro	Cys	Pro	Pro	Gly	Thr	Tyr	Ile	Ala	His		
		35				40					45						
Leu	Asn	Gly	Leu	Ser	Lys	Cys	Leu	Gln	Cys	Gln	Met	Cys	Asp	Pro	Ala		
	50					55				60							
Met	Gly	Leu	Arg	Ala	Ser	Arg	Asn	Cys	Ser	Arg	Thr	Glu	Asn	Ala	Val		
65				70					75						80		
Cys	Gly	Cys	Ser	Pro	Gly	His	Phe	Cys	Ile	Val	Gln	Asp	Gly	Asp	His		

				85					90					95					
Cys	Ala	Ala	Cys	Arg	Ala	Tyr	Ala	Thr	Ser	Ser	Pro	Gly	Gln	Arg	Val				
			100					105					110						
Gln	Lys	Gly	Gly	Thr	Glu	Ser	Gln	Asp	Thr	Leu	Cys	Gln	Asn	Cys	Pro				
		115					120					125							
Pro	Gly	Thr	Phe	Ser	Pro	Asn	Gly	Thr	Leu	Glu	Glu	Cys	Gln	His	Gln				
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Pro	Cys	Tyr	Ala	Pro	Ala														
	-5																		

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1				5				10						15					
aga	acc	gac	gtc	tcg	agg	ctg	gtg	ctg	tat	ctc	acc	ttc	ctg	gga	gcc				96
Arg	Thr	Asp	Val	Ser	Arg	Leu	Val	Leu	Tyr	Leu	Thr	Phe	Leu	Gly	Ala				
			20				25						30						
ccc	tgc	tac	gcc	cca	gct														114
Pro	Cys	Tyr	Ala	Pro	Ala														
			35																

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 <213> Homo sapiens

Cys	Lys	Glu	Asp	Glu	Tyr	Pro	Val	Gly	Ser	Glu	Cys	Cys	Pro	Lys	Cys				



<212> DNA  
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<220>  
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 ctg cag tgc caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg 96  
 Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg  
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 aac tgc tcc agg aca gag aac gcc gtg tgt 126  
 Asn Cys Ser Arg Thr Glu Asn Ala Val Cys  
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 1 5 10 15  
 gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag 96  
 Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys  
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Cys	Tyr	Ala	Pro	Ala	Leu	Pro	Ser	Cys	Lys	Glu	Asp	Glu	Tyr	Pro	Val		
	35					40					45						
ggc	tcc	gag	tgc	tgc	ccc	aag	tgc	agt	cca	ggt	tat	cgt	gtg	aag	gag	488	
Gly	Ser	Glu	Cys	Cys	Pro	Lys	Cys	Ser	Pro	Gly	Tyr	Arg	Val	Lys	Glu		
	50				55				60						65		
gcc	tgc	ggg	gag	ctg	acg	ggc	aca	gtg	tgt	gaa	ccc	tgc	cct	cca	ggc	536	
Ala	Cys	Gly	Glu	Leu	Thr	Gly	Thr	Val	Cys	Glu	Pro	Cys	Pro	Pro	Gly		
				70				75						80			
acc	tac	att	gcc	cac	ctc	aat	ggc	cta	agc	aag	tgt	ctg	cag	tgc	caa	584	
Thr	Tyr	Ile	Ala	His	Leu	Asn	Gly	Leu	Ser	Lys	Cys	Leu	Gln	Cys	Gln		
			85				90					95					
atg	tgt	gac	cca	gcc	atg	ggc	ctg	cgc	gcg	agc	cgg	aac	tgc	tcc	agg	632	
Met	Cys	Asp	Pro	Ala	Met	Gly	Leu	Arg	Ala	Ser	Arg	Asn	Cys	Ser	Arg		
		100					105					110					
aca	gag	aac	gcc	gtg	tgt	ggc	tgc	agc	cca	ggc	cac	ttc	tgc	atc	gtc	680	
Thr	Glu	Asn	Ala	Val	Cys	Gly	Cys	Ser	Pro	Gly	His	Phe	Cys	Ile	Val		
	115					120					125						
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Gln	Asp	Gly	Asp	His	Cys	Ala	Ala	Cys	Arg	Ala	Tyr	Ala	Thr	Ser	Ser		
	130				135				140						145		
ccg	ggc	cag	agg	gtg	cag	aag	gga	ggc	acc	gag	agt	cag	gac	acc	ctg	776	
Pro	Gly	Gln	Arg	Val	Gln	Lys	Gly	Gly	Thr	Glu	Ser	Gln	Asp	Thr	Leu		
				150					155					160			
tgt	cag	aac	tgc	ccc	ccg	ggg	acc	ttc	tct	ccc	aat	ggg	acc	ctg	gag	824	
Cys	Gln	Asn	Cys	Pro	Pro	Gly	Thr	Phe	Ser	Pro	Asn	Gly	Thr	Leu	Glu		
			165					170					175				
gaa	tgt	cag	cac	cag	acc	aag	tgc	agc	tgg	ctg	gtg	acg	aag	gcc	gga	872	
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gct	ggg	acc	agc	agc	tcc	cac	tgg	gta	tgg	tgg	ttt	ctc	tca	ggg	agc	920	
Ala	Gly	Thr	Ser	Ser	Ser	His	Trp	Val	Trp	Trp	Phe	Leu	Ser	Gly	Ser		
	195					200					205						
ctc	gtc	atc	gtc	att	gtt	tgc	tcc	aca	gtt	ggc	cta	atc	ata	tgt	gtg	968	
Leu	Val	Ile	Val	Ile	Val	Cys	Ser	Thr	Val	Gly	Leu	Ile	Ile	Cys	Val		
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aaa	aga	aga	aag	cca	agg	ggt	gat	gta	gtc	aag	gtg	atc	gtc	tcc	gtc	1016	
Lys	Arg	Arg	Lys	Pro	Arg	Gly	Asp	Val	Val	Lys	Val	Ile	Val	Ser	Val		
				230					235					240			
cag	cgg	aaa	aga	cag	gag	gca	gaa	ggt	gag	gcc	aca	gtc	att	gag	gcc	1064	
Gln	Arg	Lys	Arg	Gln	Glu	Ala	Glu	Gly	Glu	Ala	Thr	Val	Ile	Glu	Ala		

245	250	255	
ctg cag gcc cct ccg gac gtc acc acg gtg gcc gtg gag gag aca ata			1112
Leu Gln Ala Pro Pro Asp Val Thr Thr Val Ala Val Glu Glu Thr Ile			
260	265	270	
ccc tca ttc acg ggg agg agc cca aac cac tgacccacag actctgcacc			1162
Pro Ser Phe Thr Gly Arg Ser Pro Asn His			
275	280		
ccgacgccag agatacctgg agcgacggct gctgaaagag gctgtccacc tggcgaaacc			1222
accggagccc ggaggcttgg gggctccgcc ctgggctggc ttccgtctcc tccagtggag			1282
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		Met Glu Pro	
		1	
cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc aga acc gac			163
Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro Arg Thr Asp			
5	10	15	
gtc ttg agg ctg gtg ctg tat ctc acc ttt ctg gga gcc ccc tgc tac			211

Val	Leu	Arg	Leu	Val	Leu	Tyr	Leu	Thr	Phe	Leu	Gly	Ala	Pro	Cys	Tyr		
20					25					30					35		
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Ala	Pro	Ala	Leu	Pro	Ser	Cys	Lys	Glu	Asp	Glu	Tyr	Pro	Val	Gly	Ser		
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gag	tgc	tgc	ccc	aag	tgc	agt	cca	ggt	tat	cgt	gtg	aag	gag	gcc	tgc	307	
Glu	Cys	Cys	Pro	Lys	Cys	Ser	Pro	Gly	Tyr	Arg	Val	Lys	Glu	Ala	Cys		
			55					60					65				
ggg	gag	ctg	acg	ggc	aca	gtg	tgt	gaa	ccc	tgc	cct	cca	ggc	acc	tac	355	
Gly	Glu	Leu	Thr	Gly	Thr	Val	Cys	Glu	Pro	Cys	Pro	Pro	Gly	Thr	Tyr		
		70					75					80					
att	gcc	cac	ctc	aat	ggc	cta	agc	aag	tgt	ctg	cag	tgc	caa	atg	tgt	403	
Ile	Ala	His	Leu	Asn	Gly	Leu	Ser	Lys	Cys	Leu	Gln	Cys	Gln	Met	Cys		
	85					90					95						
gac	cca	gcc	atg	ggc	ctg	cgc	gcg	agc	cgg	aac	tgc	tcc	agg	aca	gag	451	
Asp	Pro	Ala	Met	Gly	Leu	Arg	Ala	Ser	Arg	Asn	Cys	Ser	Arg	Thr	Glu		
100					105					110					115		
aac	gcc	gtg	tgt	ggc	tgc	agc	cca	ggc	cac	ttc	tgc	atc	gtc	cag	gac	499	
Asn	Ala	Val	Cys	Gly	Cys	Ser	Pro	Gly	His	Phe	Cys	Ile	Val	Gln	Asp		
				120					125					130			
ggg	gac	cac	tgc	gcc	gcg	tgc	cgc	gct	tac	gcc	acc	tcc	agc	ccg	ggc	547	
Gly	Asp	His	Cys	Ala	Ala	Cys	Arg	Ala	Tyr	Ala	Thr	Ser	Ser	Pro	Gly		
			135					140					145				
cag	agg	gtg	cag	aag	gga	ggc	acc	gag	agt	cag	gac	acc	ctg	tgt	cag	595	
Gln	Arg	Val	Gln	Lys	Gly	Gly	Thr	Glu	Ser	Gln	Asp	Thr	Leu	Cys	Gln		
		150					155					160					
aac	tgc	ccc	ccg	ggg	acc	ttc	tct	ccc	aat	ggg	acc	ctg	gag	gaa	tgt	643	
Asn	Cys	Pro	Pro	Gly	Thr	Phe	Ser	Pro	Asn	Gly	Thr	Leu	Glu	Glu	Cys		
	165					170					175						
cag	cac	cag	acc	aat	tgg	cct	aat	cat	atg	tgt	gaa	aag	aag	aaa	gcc	691	
Gln	His	Gln	Thr	Asn	Trp	Pro	Asn	His	Met	Cys	Glu	Lys	Lys	Lys	Ala		
180					185				190						195		
aag	ggg	tgagcacacg	gcggcccat	cagggtcat	gtccccagcc	gtcacctctt										747	
Lys	Gly																
ggagctctgt	caccccaagc	ctgggaggtg	gccccagagc	ttttccagga	tccgcggctc											807	
ctcccagggc	agccactgca	ggctgggggca	ggtgatgtag	tcaaggtgat	cgtctccatc											867	
cagcggaana	gacaggaggc	agaaggtgag	gccacagtca	ttgaggccct	gcaggccctc											927	
ccggacgtca	ccacggtggc	cgtggaggag	acaataccct	cattcacggg	gaggagccca											987	
aaccactgac	ccacagactc	tgcaccccg	cgccagagat	acctggagcg	acggctgctg											1047	
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gacgccacgt	gccattccca	tggggccagt	agggcctggg	gcctctgttc	tgctgtggcc											1227	
tgagctcccc	agagtcttga	ggaggagcgc	cagttgcccc	tcgctcacag	accacacacc											1287	
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gctgcagtgt	ggtgttttagt	ggataaccaca	tcggaagtga	ttttctaaat	tggatttgaa	1467
ttcggctcct	gtttttctatt	tgatcatgaaa	cagtgtattt	ggggagatgc	tgtgggagga	1527
tgtaaataatc	ttgtttctcc	tcaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa	1587
aaaaaaaaaa						1596

<210> 18  
 <211> 197  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> (1)...(38)

<400> 18																	
Met	Glu	Pro	Pro	Gly	Asp	Trp	Gly	Pro	Pro	Pro	Trp	Arg	Ser	Thr	Pro		
			-35					-30					-25				
Arg	Thr	Asp	Val	Leu	Arg	Leu	Val	Leu	Tyr	Leu	Thr	Phe	Leu	Gly	Ala		
		-20					-15					-10					
Pro	Cys	Tyr	Ala	Pro	Ala	Leu	Pro	Ser	Cys	Lys	Glu	Asp	Glu	Tyr	Pro		
	-5					1				5					10		
Val	Gly	Ser	Glu	Cys	Cys	Pro	Lys	Cys	Ser	Pro	Gly	Tyr	Arg	Val	Lys		
			15					20					25				
Glu	Ala	Cys	Gly	Glu	Leu	Thr	Gly	Thr	Val	Cys	Glu	Pro	Cys	Pro	Pro		
			30				35						40				
Gly	Thr	Tyr	Ile	Ala	His	Leu	Asn	Gly	Leu	Ser	Lys	Cys	Leu	Gln	Cys		
		45				50					55						
Gln	Met	Cys	Asp	Pro	Ala	Met	Gly	Leu	Arg	Ala	Ser	Arg	Asn	Cys	Ser		
	60					65					70						
Arg	Thr	Glu	Asn	Ala	Val	Cys	Gly	Cys	Ser	Pro	Gly	His	Phe	Cys	Ile		
	75				80					85					90		
Val	Gln	Asp	Gly	Asp	His	Cys	Ala	Ala	Cys	Arg	Ala	Tyr	Ala	Thr	Ser		
				95					100					105			
Ser	Pro	Gly	Gln	Arg	Val	Gln	Lys	Gly	Thr	Glu	Ser	Gln	Asp	Thr			
		110						115				120					
Leu	Cys	Gln	Asn	Cys	Pro	Pro	Gly	Thr	Phe	Ser	Pro	Asn	Gly	Thr	Leu		
		125					130					135					
Glu	Glu	Cys	Gln	His	Gln	Thr	Asn	Trp	Pro	Asn	His	Met	Cys	Glu	Lys		
	140					145					150						
Lys	Lys	Ala	Lys	Gly													
155																	

<210> 19  
 <211> 591  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(591)

<400> 19																		
atg	gag	cct	cct	gga	gac	tgg	ggg	cct	cct	ccc	tgg	aga	tcc	acc	ccc			
Met	Glu	Pro	Pro	Gly	Asp	Trp	Gly	Pro	Pro	Pro	Trp	Arg	Ser	Thr	Pro		48	
1				5					10					15				

aga acc gac gtc ttg agg ctg gtg ctg tat ctc acc ttt ctg gga gcc	96
Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala	
20 25 30	
ccc tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca	144
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro	
35 40 45	
gtg ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag	192
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys	
50 55 60	
gag gcc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca	240
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro	
65 70 75 80	
ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc	288
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys	
85 90 95	
caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc	336
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser	
100 105 110	
agg aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc	384
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile	
115 120 125	
gtc cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc	432
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser	
130 135 140	
agc ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc	480
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr	
145 150 155 160	
ctg tgt cag aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg	528
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu	
165 170 175	
gag gaa tgt cag cac cag acc aat tgg cct aat cat atg tgt gaa aag	576
Glu Glu Cys Gln His Gln Thr Asn Trp Pro Asn His Met Cys Glu Lys	
180 185 190	
aag aaa gcc aag ggg	591
Lys Lys Ala Lys Gly	
195	

<210> 20  
 <211> 159  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
 Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys  
 1 5 10 15

Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu  
20 25 30  
Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His  
35 40 45  
Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala  
50 55 60  
Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val  
65 70 75 80  
Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His  
85 90 95  
Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val  
100 105 110  
Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro  
115 120 125  
Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln  
130 135 140  
Thr Asn Trp Pro Asn His Met Cys Glu Lys Lys Lys Ala Lys Gly  
145 150 155

<210> 21  
<211> 38  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> (1)...(38)

<400> 21  
Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro  
-35 -30 -25  
Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala  
-20 -15 -10  
Pro Cys Tyr Ala Pro Ala  
-5

<210> 22  
<211> 114  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)...(114)

<400> 22  
atg gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc 48  
Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro  
1 5 10 15  
aga acc gac gtc tcg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc 96  
Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala  
20 25 30  
ccc tgc tac gcc cca gct 114  
Pro Cys Tyr Ala Pro Ala  
35

<210> 23  
 <211> 34  
 <212> PRT  
 <213> Homo sapiens

<400> 23  
 Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys Cys  
 1 5 10 15  
 Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr  
 20 25 30  
 Val Cys

<210> 24  
 <211> 42  
 <212> PRT  
 <213> Homo sapiens

<400> 24  
 Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys  
 1 5 10 15  
 Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg  
 20 25 30  
 Asn Cys Ser Arg Thr Glu Asn Ala Val Cys  
 35 40

<210> 25  
 <211> 42  
 <212> PRT  
 <213> Homo sapiens

<400> 25  
 Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala  
 1 5 10 15  
 Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys  
 20 25 30  
 Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys  
 35 40

<210> 26  
 <211> 105  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(105)

<400> 26  
 tcc tgc aag gag gac gag tac cca gtg ggc tcc gag tgc tgc ccc aag 48  
 Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys  
 1 5 10 15  
 tgc agt cca ggt tat cgt gtg aag gag gcc tgc ggg gag ctg acg ggc 96  
 Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly

	20	25	30	
aca gtg tgt				105
Thr Val Cys				
35				
<210>	27			
<211>	126			
<212>	DNA			
<213>	Homo sapiens			
<220>				
<221>	CDS			
<222>	(1)...(126)			
<400>	27			
tgc cct cca ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt				48
Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys				
1 5 10 15				
ctg cag tgc caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg				96
Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg				
20 25 30				
aac tgc tcc agg aca gag aac gcc gtg tgt				126
Asn Cys Ser Arg Thr Glu Asn Ala Val Cys				
35 40				
<210>	28			
<211>	126			
<212>	DNA			
<213>	Homo sapiens			
<220>				
<221>	CDS			
<222>	(1)...(126)			
<400>	28			
tgc agc cca ggc cac ttc tgc atc gtc cag gac ggg gac cac tgc gcc				48
Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala				
1 5 10 15				
gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag				96
Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys				
20 25 30				
gga ggc acc gag agt cag gac acc ctg tgt				126
Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys				
35 40				
<210>	29			
<211>	2313			
<212>	DNA			
<213>	Homo sapiens			



<220>  
 <221> CDS  
 <222> (85)...(642)

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<400> 29
gtcgacccac gcgtccggct gagttcctct gctggagttc atcctgctag ctgggttccc      60
gagctgccgg tctgagcctg aggc atg gag cct cct gga gac tgg ggg cct      111
                Met Glu Pro Pro Gly Asp Trp Gly Pro
                  1                      5

cct ccc tgg aga tcc acc ccc aga acc gac gtc tgc agg ctg gtg ctg      159
Pro Pro Trp Arg Ser Thr Pro Arg Thr Asp Val Ser Arg Leu Val Leu
 10                      15                      20                      25

tat ctc acc ttc ctg gga gcc ccc tgc tac gcc cca gct ctg ccg tcc      207
Tyr Leu Thr Phe Leu Gly Ala Pro Cys Tyr Ala Pro Ala Leu Pro Ser
                30                      35                      40

tgc aag gag gac gag tac cca gtg ggc tcc gag tgc tgc ccc aag tgc      255
Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys Cys
                45                      50                      55

agt cca ggt tat cgt gtg aag gag gcc tgc ggg gag ctg acg ggc aca      303
Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr
                60                      65                      70

gtg tgt gaa ccc tgc cct cca ggc acc tac att gcc cac ctc aat ggc      351
Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly
 75                      80                      85

cta agc aag tgt ctg cag tgc caa atg tgt gac cca gcc atg ggc ctg      399
Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu
 90                      95                      100                      105

cgc gcg agc cgg aac tgc tcc agg aca gag aac gcc gtg tgt ggc tgc      447
Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val Cys Gly Cys
                110                      115                      120

agc cca ggc cac ttc tgc atc gtc cag gac ggg gac cac tgc gcc gcg      495
Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala Ala
                125                      130                      135

tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag gga      543
Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys Gly
 140                      145                      150

ggc acc gag agt cag gac acc ctg tgt cag aac tgc ccc ccg ggg acc      591
Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro Pro Gly Thr
 155                      160                      165

ttc tct ccc aat ggg acc ctg gag gaa tgt cag cac cag acc aaa aag      639
Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln Thr Lys Lys
 170                      175                      180                      185

gct tgaaggtccc accctgagcg gcaccctggt cacatgcctg cgtccaggag      692
Ala

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agctgcaggg ctgaagcctg tgtgccccag ataaccctt ccatggggccc agacaaagcc 752
tcatacagatc tgagcttcct ggaggctcag gatgggcctt cccagaagca ggcccagagg 812
gaggctgcct ccagatcccc tgtcccctgg ggctgtgggt gtccctgaat gtcaggggcca 872
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agtcctgtcc atctccagct ctaaccattt ttgtcccagc actggctctc cctctacctt 1172
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cattgtttgc tccacagttg gcctaatacat atgtgtgaaa agaagaaagc caaggggtga 1652
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agtcattgag gccctgcagg cccctccgga cgtcaccacg gtggccgtgg aggagacaat 1772
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gggcccctgc tggggtagag ctggggacgc cacgtgccat tcccatgggc cagtgagggc 2012
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gcccctcgtc cacagaccac acaccagcc ctctggggc agcccagagg gcccttcaga 2132
ccccagctgt ctgcgcgtct gactcttgtg gcctcagcag gacaggcccc gggcactgcc 2192
tcacagccaa ggctggactg ggttggctgc agtgtggtgt ttagtgata ccacatcgga 2252
agtgattttc taaattggat ttgaattcgg aaaaaaaaaa aaaaaaaaaa agggcgggcg 2312
c 2313

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<210> 30
<211> 186
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> (1)...(38)

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<400> 30
Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
-35 -30 -25
Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
-20 -15 -10
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
-5 1 5 10
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
15 20 25
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
30 35 40
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
45 50 55
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
60 65 70
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
75 80 85 90

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Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser  
95 100 105  
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr  
110 115 120  
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu  
125 130 135  
Glu Glu Cys Gln His Gln Thr Lys Lys Ala  
140 145

<210> 31  
<211> 558  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)...(558)

<400> 31  
atg gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc 48  
Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro  
1 5 10 15  
aga acc gac gtc tgc agg ctg gtg ctg tat ctc acc ttc ctg gga gcc 96  
Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala  
20 25 30  
ccc tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca 144  
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro  
35 40 45  
gtg ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag 192  
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys  
50 55 60  
gag gcc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca 240  
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro  
65 70 75 80  
ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc 288  
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys  
85 90 95  
caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc 336  
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser  
100 105 110  
agg aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc 384  
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile  
115 120 125  
gtc cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc 432  
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser  
130 135 140  
agc ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc 480  
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr

145		150		155		160	
ctg tgt cag aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg							528
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu							
	165			170		175	

gag gaa tgt cag cac cag acc aaa aag gct							558
Glu Glu Cys Gln His Gln Thr Lys Lys Ala							
	180			185			

<210> 32  
 <211> 148  
 <212> PRT  
 <213> Homo sapiens

<400> 32

Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys																
1			5					10					15			
Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu																
	20						25						30			
Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His																
	35						40						45			
Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala																
	50					55				60						
Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val																
65					70				75							80
Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His																
			85					90								95
Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val																
	100						105							110		
Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro																
	115						120							125		
Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln																
	130					135								140		
Thr Lys Lys Ala																
145																

<210> 33  
 <211> 38  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> (1)...(38)

<400> 33

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	-35							-30						-25		
Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala																
	-20						-15							-10		
Pro Cys Tyr Ala Pro Ala																
	-5															

<210> 34  
 <211> 114

<212> DNA  
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<220>  
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 <222> (1)...(114)

<400> 34  
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 Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro  
 1 5 10 15  
 aga acc gac gtc tcg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc 96  
 Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala  
 20 25 30  
 ccc tgc tac gcc cca gct 114  
 Pro Cys Tyr Ala Pro Ala  
 35

<210> 35  
 <211> 34  
 <212> PRT  
 <213> Homo sapiens

<400> 35  
 Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys Cys  
 1 5 10 15  
 Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr  
 20 25 30  
 Val Cys

<210> 36  
 <211> 42  
 <212> PRT  
 <213> Homo sapiens

<400> 36  
 Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys  
 1 5 10 15  
 Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg  
 20 25 30  
 Asn Cys Ser Arg Thr Glu Asn Ala Val Cys  
 35 40

<210> 37  
 <211> 42  
 <212> PRT  
 <213> Homo sapiens

<400> 37  
 Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala  
 1 5 10 15  
 Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys  
 20 25 30

Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys  
 35 40

<210> 38  
 <211> 105  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (1)...(105)

<400> 38

tcc tgc aag gag gac gag tac cca gtg ggc tcc gag tgc tgc ccc aag	48
Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys	
1 5 10 15	

tgc agt cca ggt tat cgt gtg aag gag gcc tgc ggg gag ctg acg ggc	96
Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly	
20 25 30	

aca gtg tgt	105
Thr Val Cys	
35	

<210> 39  
 <211> 126  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(126)

<400> 39

tgc cct cca ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt	48
Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys	
1 5 10 15	

ctg cag tgc caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg	96
Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg	
20 25 30	

aac tgc tcc agg aca gag aac gcc gtg tgt	126
Asn Cys Ser Arg Thr Glu Asn Ala Val Cys	
35 40	

<210> 40  
 <211> 126  
 <212> DNA  
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<220>  
 <221> CDS  
 <222> (1)...(126)

<400> 40  
tgc agc cca ggc cac ttc tgc atc gtc cag gac ggg gac cac tgc gcc 48  
Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala  
1 5 10 15

gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag 96  
Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys  
20 25 30

gga ggc acc gag agt cag gac acc ctg tgt 126  
Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys  
35 40

<210> 41  
<211> 1834  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (103)...(933)

<400> 41  
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cctgctagct gggttcccga gctgccggtc tgagcctgag gc atg gag cct cct 114  
Met Glu Pro Pro  
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gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc aga acc gac gtc 162  
Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro Arg Thr Asp Val  
5 10 15 20

ttg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc ccc tgc tac gcc 210  
Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala Pro Cys Tyr Ala  
25 30 35

cca gct ctg ccg tcc tgc aag gag gac gag tac cca gtg ggc tcc gag 258  
Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu  
40 45 50

tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag gag gcc tgc ggg 306  
Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly  
55 60 65

gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca ggc acc tac att 354  
Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile  
70 75 80

gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc caa atg tgt gac 402  
Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp  
85 90 95 100

cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc agg aca gag aac 450  
Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn  
105 110 115

gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc gtc cag gac ggg Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly 120 125 130	498
gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln 135 140 145	546
agg gtg cag aag gga ggc acc gag agt cag gac acc ctg tgt cag aac Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn 150 155 160	594
tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg gag gaa tgt cag Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln 165 170 175 180	642
cac cag acc aag tgc agc tgg ctg gtg acg aag gcc gga gct ggg acc His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala Gly Ala Gly Thr 185 190 195	690
agc agc tcc cac tgg gta tgg tgg ttt ctc tca ggg agc ctc gtc atc Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly Ser Leu Val Ile 200 205 210	738
gtc att gtt tgc tcc aca gtt ggc cta atc ata tgt gtg aaa aga aga Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys Val Lys Arg Arg 215 220 225	786
aag cca agg ggt gat gta gtc aag gtg atc gtc tcc gtc cag gta ttg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser Val Gln Val Leu 230 235 240	834
atc ctc ctc ccc ctc tcc ctc ccc cct cca cct tcc cac ctc ccc tct Ile Leu Leu Pro Leu Ser Leu Pro Pro Pro Pro Ser His Leu Pro Ser 245 250 255 260	882
ccc cgc tgg ggc tgg tgt ttc tgg tgt aca tgg tgg ggg ctc cca gtt Pro Arg Trp Gly Trp Cys Phe Trp Cys Thr Trp Trp Gly Leu Pro Val 265 270 275	930
ctc tgagggtcct gagtctttca agtacagcca cggtagctca ggaaagaacc Leu	983
cacccccctca aactgaaagc agtaaaatga acccgagaac ctggagtccc agggggggcct gagcaggcag ggtctccacg attcgtgtgc tcacagcgga aaagacagga ggcagaaggt gaggccacag tcattgaggc cctgcaggcc cctccggacg tcaccacggt ggccgtggag gagacaatac cctcattcac ggggaggagc ccaaaccact gacccacaga ctctgcaccc cgacgccaga gatacctgga gcgacggctg ctgaaagagg ctgtccacct ggcgaaacca ccggagccccg gaggcttggg ggctccgccc tgggctggct tccgtctcct ccagtggagg gagaggtggg gcccctgctg gggtagagct ggggacgcca cgtgccattc ccatgggcca gtgagggcct ggggcctctg ttctgctgtg gcctgagctc cccagagtcc tgaggaggag cgccagttgc ccctcgctca cagaccacac acccagccct cctgggcccag cccagagggc ccttcagacc ccagctgtct gcgctgtga ctcttgtggc ctcagcagga caggccccg gcactgcctc acagccaagg ctggactggg ttggctgcag tgttgtgttt agtggatacc acatcggaag tgattttcta aattggattt gaattcggct cctgttttct atttgtcatg	1043 1103 1163 1223 1283 1343 1403 1463 1523 1583 1643 1703



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aaacagtgtgta tttgggggaga tgctgtggga ggatgtaaat atcttgtttc tcctcaaaaa 1763
aaaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1823
agggcggccg c 1834

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<210> 42
<211> 277
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> (1)...(38)

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<400> 42
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-35 -30 -25
Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
-20 -15 -10
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
-5 1 5 10
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
15 20 25
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
30 35 40
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
45 50 55
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
60 65 70
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
75 80 85 90
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
95 100 105
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
110 115 120
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
125 130 135
Glu Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala
140 145 150
Gly Ala Gly Thr Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly
155 160 165 170
Ser Leu Val Ile Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys
175 180 185
Val Lys Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser
190 195 200
Val Gln Val Leu Ile Leu Leu Pro Leu Ser Leu Pro Pro Pro Pro Ser
205 210 215
His Leu Pro Ser Pro Arg Trp Gly Trp Cys Phe Trp Cys Thr Trp Trp
220 225 230
Gly Leu Pro Val Leu
235

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<210> 43
<211> 831
<212> DNA
<213> Homo sapiens

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<220>

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<221> CDS

<222> (1)...(831)

<400> 43

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Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro	
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aga acc gac gtc ttg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc	96
Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala	
20 25 30	
ccc tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca	144
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro	
35 40 45	
gtg ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag	192
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Ggt Tyr Arg Val Lys	
50 55 60	
gag gcc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca	240
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro	
65 70 75 80	
ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc	288
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys	
85 90 95	
caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc	336
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser	
100 105 110	
agg aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc	384
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile	
115 120 125	
gtc cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc	432
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser	
130 135 140	
agc ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc	480
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr	
145 150 155 160	
ctg tgt cag aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg	528
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu	
165 170 175	
gag gaa tgt cag cac cag acc aag tgc agc tgg ctg gtg acg aag gcc	576
Glu Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala	
180 185 190	
gga gct ggg acc agc agc tcc cac tgg gta tgg tgg ttt ctc tca ggg	624
Gly Ala Gly Thr Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly	
195 200 205	
agc ctc gtc atc gtc att gtt tgc tcc aca gtt ggc cta atc ata tgt	672

Ser	Leu	Val	Ile	Val	Ile	Val	Cys	Ser	Thr	Val	Gly	Leu	Ile	Ile	Cys	
210						215					220					
gtg	aaa	aga	aga	aag	cca	agg	ggg	gat	gta	gtc	aag	gtg	atc	gtc	tcc	720
Val	Lys	Arg	Arg	Lys	Pro	Arg	Gly	Asp	Val	Val	Lys	Val	Ile	Val	Ser	
225					230					235					240	
gtc	cag	gta	ttg	atc	ctc	ctc	ccc	ctc	tcc	ctc	ccc	cct	cca	cct	tcc	768
Val	Gln	Val	Leu	Ile	Leu	Leu	Pro	Leu	Ser	Leu	Pro	Pro	Pro	Pro	Ser	
				245					250					255		
cac	ctc	ccc	tct	ccc	cgc	tgg	ggc	tgg	tgt	ttc	tgg	tgt	aca	tgg	tgg	816
His	Leu	Pro	Ser	Pro	Arg	Trp	Gly	Trp	Cys	Phe	Trp	Cys	Thr	Trp	Trp	
			260					265					270			
ggg	ctc	cca	gtt	ctc												831
Gly	Leu	Pro	Val	Leu												
				275												

<210> 44  
 <211> 239  
 <212> PRT  
 <213> Homo sapiens

<400> 44

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Pro	Lys	Cys	Ser	Pro	Gly	Tyr	Arg	Val	Lys	Glu	Ala	Cys	Gly	Glu	Leu	
			20					25					30			
Thr	Gly	Thr	Val	Cys	Glu	Pro	Cys	Pro	Pro	Gly	Thr	Tyr	Ile	Ala	His	
			35				40					45				
Leu	Asn	Gly	Leu	Ser	Lys	Cys	Leu	Gln	Cys	Gln	Met	Cys	Asp	Pro	Ala	
	50					55				60						
Met	Gly	Leu	Arg	Ala	Ser	Arg	Asn	Cys	Ser	Arg	Thr	Glu	Asn	Ala	Val	
65					70					75					80	
Cys	Gly	Cys	Ser	Pro	Gly	His	Phe	Cys	Ile	Val	Gln	Asp	Gly	Asp	His	
				85					90					95		
Cys	Ala	Ala	Cys	Arg	Ala	Tyr	Ala	Thr	Ser	Ser	Pro	Gly	Gln	Arg	Val	
			100					105					110			
Gln	Lys	Gly	Gly	Thr	Glu	Ser	Gln	Asp	Thr	Leu	Cys	Gln	Asn	Cys	Pro	
	115						120					125				
Pro	Gly	Thr	Phe	Ser	Pro	Asn	Gly	Thr	Leu	Glu	Glu	Cys	Gln	His	Gln	
	130					135					140					
Thr	Lys	Cys	Ser	Trp	Leu	Val	Thr	Lys	Ala	Gly	Ala	Gly	Thr	Ser	Ser	
145					150					155					160	
Ser	His	Trp	Val	Trp	Trp	Phe	Leu	Ser	Gly	Ser	Leu	Val	Ile	Val	Ile	
				165					170					175		
Val	Cys	Ser	Thr	Val	Gly	Leu	Ile	Ile	Cys	Val	Lys	Arg	Arg	Lys	Pro	
			180					185					190			
Arg	Gly	Asp	Val	Val	Lys	Val	Ile	Val	Ser	Val	Gln	Val	Leu	Ile	Leu	
	195						200					205				
Leu	Pro	Leu	Ser	Leu	Pro	Pro	Pro	Pro	Ser	His	Leu	Pro	Ser	Pro	Arg	
	210					215					220					
Trp	Gly	Trp	Cys	Phe	Trp	Cys	Thr	Trp	Trp	Gly	Leu	Pro	Val	Leu		
225					230					235						

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<220>
<221> SIGNAL
<222> (1) ... (38)
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<210> 46
<211> 114
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1) ... (114)
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<210> 47
<211> 34
<212> PRT
<213> Homo sapiens
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<210> 48
<211> 42
<212> PRT
<213> Homo sapiens
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<400> 48  
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 20 25 30  
 Asn Cys Ser Arg Thr Glu Asn Ala Val Cys  
 35 40

<210> 49  
 <211> 42  
 <212> PRT  
 <213> Homo sapiens

<400> 49  
 Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala  
 1 5 10 15  
 Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys  
 20 25 30  
 Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys  
 35 40

<210> 50  
 <211> 22  
 <212> PRT  
 <213> Homo sapiens

<400> 50  
 Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln  
 1 5 10 15  
 His Gln Thr Lys Cys Ser  
 20

<210> 51  
 <211> 25  
 <212> PRT  
 <213> Homo sapiens

<400> 51  
 Trp Val Trp Trp Phe Leu Ser Gly Ser Leu Val Ile Val Ile Val Cys  
 1 5 10 15  
 Ser Thr Val Gly Leu Ile Ile Cys Val  
 20 25

<210> 52  
 <211> 105  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(105)

<400> 52  
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 Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys  
 1 5 10 15

48

tgc agt cca ggt tat cgt gtg aag gag gcc tgc ggg gag ctg acg ggc	96
Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly	
20 25 30	

aca gtg tgt	105
Thr Val Cys	
35	

<210> 53  
 <211> 126  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(126)

<400> 53	
tgc cct cca ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt	48
Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys	
1 5 10 15	

ctg cag tgc caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg	96
Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg	
20 25 30	

aac tgc tcc agg aca gag aac gcc gtg tgt	126
Asn Cys Ser Arg Thr Glu Asn Ala Val Cys	
35 40	

<210> 54  
 <211> 126  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(126)

<400> 54	
tgc agc cca ggc cac ttc tgc atc gtc cag gac ggg gac cac tgc gcc	48
Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala	
1 5 10 15	

gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag	96
Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys	
20 25 30	

gga ggc acc gag agt cag gac acc ctg tgt	126
Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys	
35 40	

<210> 55

<211> 66  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(66)

<400> 55  
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 1 5 10 15  
 cac cag acc aag tgc agc 66  
 His Gln Thr Lys Cys Ser  
 20

<210> 56  
 <211> 75  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (1)...(75)

<400> 56  
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 Trp Val Trp Trp Phe Leu Ser Gly Ser Leu Val Ile Val Ile Val Cys  
 1 5 10 15  
 tcc aca gtt ggc cta atc ata tgt gtg 75  
 Ser Thr Val Gly Leu Ile Ile Cys Val  
 20 25

<210> 57  
 <211> 32  
 <212> DNA  
 <213> Homo sapiens

<220>

<400> 57  
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<210> 58  
 <211> 39  
 <212> DNA  
 <213> Homo sapiens

<220>

<400> 58  
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Input file T198sHVEM1; Output File T198sHVEM1.pat  
Sequence length 1929

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CCACCCAGCAGGCCTGAGCCCCCTCTGCTGCCAGACCCCCTGCTGCCCACTCTCCTGCTGCTCGGGTTCTGAGGCA 158
CAGCTTGTCACACCCAGGCGGATTCTCTTTCTCTTTCTCTTTCTCTTCTGCCCCACAGCCGCAGCAATGGCGCTGAGTT 237
CCTCTGCTGGAGTTCATCCTGCTAGCTGGGTTCCCCGAGCTGCCGGTCTGAGCCTGAGGC M E P P G 5
ATG GAG CCT CCT GGA 311
D W G P P P W R S T P R T D V L R L V L 25
GAC TGG GGG CCT CCT CCC TGG AGA TCC ACC CCC AGA ACC GAC GTC TTG AGG CTG GTG CTG 371
Y L T F L G A P C Y A P A L P S C K E D 45
TAT CTC ACC TTC CTG GGA GCC CCC TGC TAC GCC CCA GCT CTG CCG TCC TGC AAG GAG GAC 431
E Y P V G S E C C P K C S P G Y R V K E 65
GAG TAC CCA GTG GGC TCC GAG TGC TGC CCC AAG TGC AGT CCA GGT TAT CGT GTG AAG GAG 491
A C G E L T G T V C E P C P P G T Y I A 85
GCC TGC GGG GAG CTG ACG GGC ACA GTG TGT GAA CCC TGC CCT CCA GGC ACC TAC ATT GCC 551
H L N G L S K C L Q C Q M C D P A M G L 105
CAC CTC AAT GGC CTA AGC AAG TGT CTG CAG TGC CAA ATG TGT GAC CCA GCC ATG GGC CTG 611
R A S R N C S R T E N A V C G C S P G H 125
CGC GCG AGC CGG AAC TGC TCC AGG ACA GAG AAC GCC GTG TGT GGC TGC AGC CCA GGC CAC 671
F C I V Q D G D H C A A C R A Y A T S S 145
TTC TGC ATC GTC CAG GAC GGG GAC CAC TGC GCC GCG TGC CGC GCT TAC GCC ACC TCC AGC 731
P G Q R V Q K G G T E S Q D T L C Q N C 165
CCG GGC CAG AGG GTG CAG AAG GGA GGC ACC GAG AGT CAG GAC ACC CTG TGT CAG AAC TGC 791
P P G T F S P N G T L E E C Q H Q T N R 185
CCC CCG GGG ACC TTC TCT CCC AAT GGG ACC CTG GAG GAA TGT CAG CAC CAG ACC AAC CGA 851
A W K S Q T D L * 194
GCT TGG AAA AGT CAG ACA GAC CTC TGA 878
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*Figure 1*





Input file T198sHVEM2; Output File T198sHVEM2.pat  
Sequence length 1596

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S   T   P   R   T   D   V   L   R   L   V   L   Y   L   T   F   L   G   A   P   33
TCC ACC CCC AGA ACC GAC GTC TTG AGG CTG GTG CTG TAT CTC ACC TTT CTG GGA GCC CCC 205

C   Y   A   P   A   L   P   S   C   K   E   D   E   Y   P   V   G   S   E   C   53
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C   P   K   C   S   P   G   Y   R   V   K   E   A   C   G   E   L   T   G   T   73
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V   C   E   P   C   P   P   G   T   Y   I   A   H   L   N   G   L   S   K   C   93
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K   A   K   G   *   198
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Figure 3

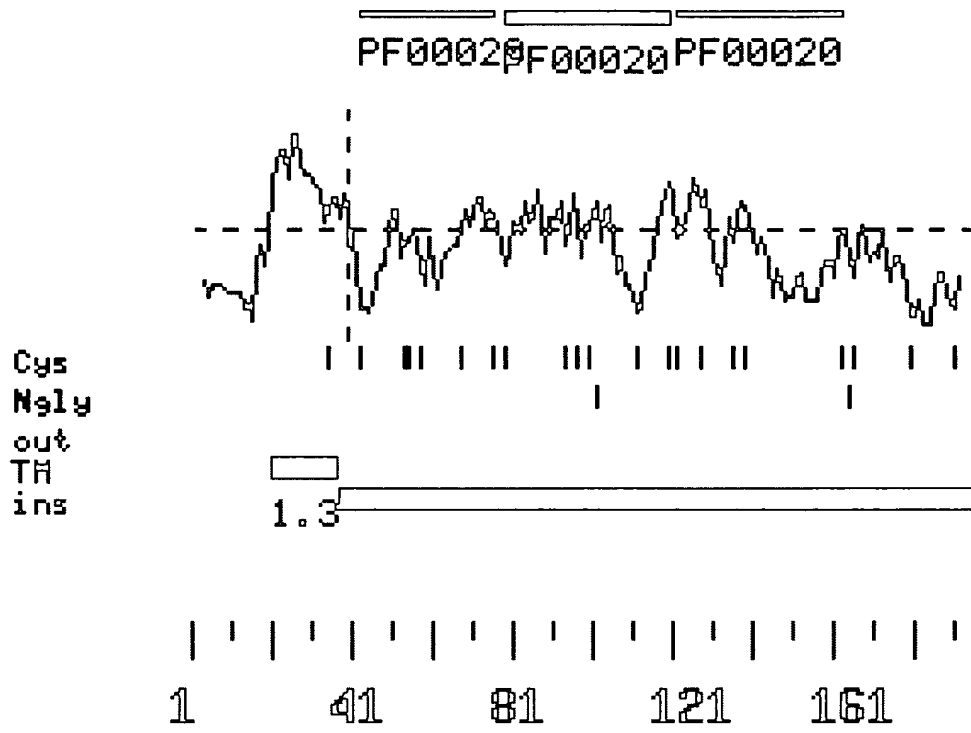


Figure 4

Input file sHVEM3; Output File sHVEM3.pat  
Sequence length 2313

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      D   V   S   R   L   V   L   Y   L   T   F   L   G   A   P   C   Y   A   P   A   38
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      L   P   S   C   K   E   D   E   Y   P   V   G   S   E   C   C   P   K   C   S   58
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      D   T   L   C   Q   N   C   P   P   G   T   F   S   P   N   G   T   L   E   E   178
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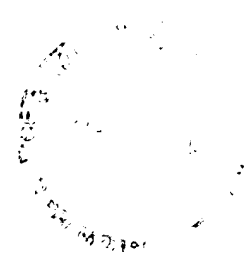
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Figure 5







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TH  
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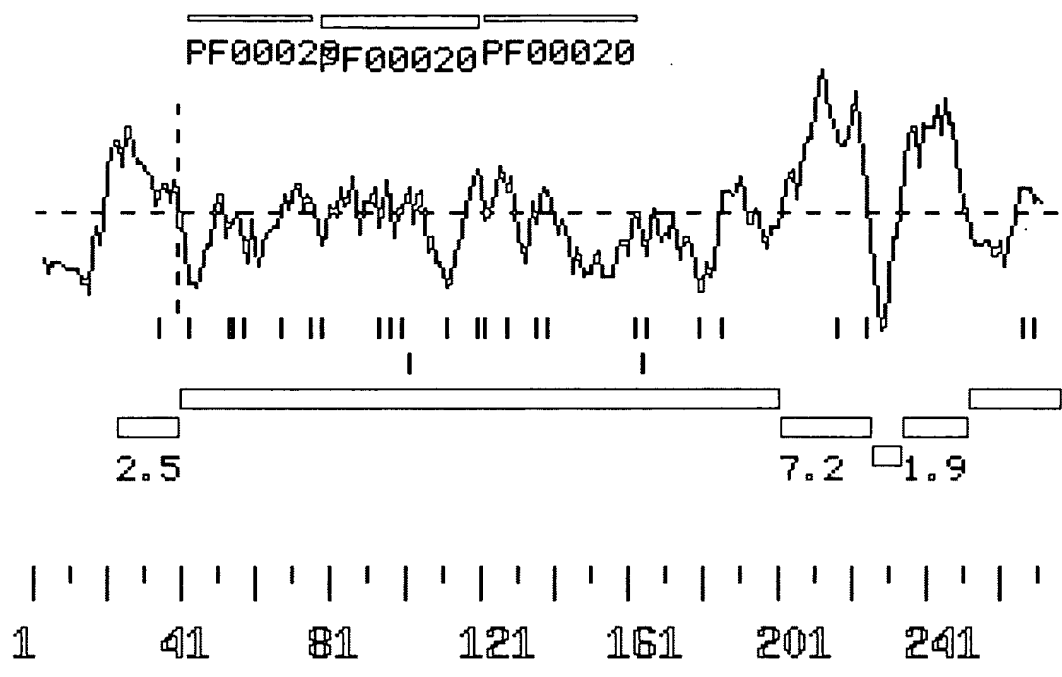


Figure 8

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Figure 9C

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2904

Figure 9D

shVEM_1_a.a.	1	MEPPGDWGPPPWSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	80
shVEM_2_a.a.		MEPPGDWGPPPWSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	
shVEM_3_a.a.		MEPPGDWGPPPWSTPRTDVSRVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	
mHVEM_2_a.a.		MEPPGDWGPPPWSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	
mHVEM__pub.__a.a.		MEPPGDWGPPPWSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	
shVEM_1_a.a.	81	GTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT	160
shVEM_2_a.a.		GTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT	
shVEM_3_a.a.		GTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT	
mHVEM_2_a.a.		GTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT	
mHVEM__pub.__a.a.		GTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDT	
shVEM_1_a.a.	161	LCQNCPPGTFSPNGTLEECQHQTNRWKSQTDL-----	240
shVEM_2_a.a.		LCQNCPPGTFSPNGTLEECQHQTNPWPNHMEKKKAG-----	
shVEM_3_a.a.		LCQNCPPGTFSPNGTLEECQHQTTKA-----	
mHVEM_2_a.a.		LCQNCPPGTFSPNGTLEECQHQTCKSWLVTKAGAGTSSSHVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS	
mHVEM__pub.__a.a.		LCQNCPPGTFSPNGTLEECQHQTCKSWLVTKAGAGTSSSHVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS	
shVEM_1_a.a.	241	-----	283
shVEM_2_a.a.		-----	
shVEM_3_a.a.		-----	
mHVEM_2_a.a.		VQVLILLPLSLPPPSHLPSPRWGWCFTWWGLPVL-----	
mHVEM__pub.__a.a.		VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH	

**Figure 10**